OIPE

#9

RAW SEQUENCE LISTING       DATE: 06/28/2001
PATENT APPLICATION: **US/09/509,648**    TIME: 13:59:49

Input Set : **A:\Cbm-691.app**
Output Set: **N:\CRF3\06282001\I509648.raw**

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See p.5

```
 3 <110> APPLICANT: Charette, Marc F.
 4        Rueger, David C.
 5        Higgins, Dennis
 7 <120> TITLE OF INVENTION: ENHANCEMENT OF MORPHOGEN ACTIVITY
 9 <130> FILE REFERENCE: 00960-569 NATL
11 <140> CURRENT APPLICATION NUMBER: 09/509,648
12 <141> CURRENT FILING DATE: 2000-10-05
14 <150> PRIOR APPLICATION NUMBER: PCT/US98/22655
15 <151> PRIOR FILING DATE: 1998-10-26
17 <150> PRIOR APPLICATION NUMBER: 60/063,624
18 <151> PRIOR FILING DATE: 1997-10-27
20 <160> NUMBER OF SEQ ID NOS: 9
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1822
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (49)..(1341)
33 <400> SEQUENCE: 1
34 ggtgcgggcc cggagcccgg agcccgggta gcgcgtagag ccggcgcg atg cac gtg   57
35                                                         Met His Val
36                                                          1
38 cgc tca ctg cga gct gcg gcg ccg cac agc ttc gtg gcg ctc tgg gca  105
39 Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
40       5                  10                  15
42 ccc ctg ttc ctg ctg cgc tcc gcc ctg gcc gac ttc agc ctg gac aac  153
43 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
44   20                  25                  30                  35
46 gag gtg cac tcg agc ttc atc cac cgg cgc ctc cgc agc cag gag cgg  201
47 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
48                  40                  45                  50
50 cgg gag atg cag cgc gag atc ctc tcc att ttg ggc ttg ccc cac cgc  249
51 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
52                  55                  60                  65
54 ccg cgc ccg cac ctc cag ggc aag cac aac tcg gca ccc atg ttc atg  297
55 Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
56          70                  75                  80
58 ctg gac ctg tac aac gcc atg gcg gtg gag gag ggc ggc ggg ccc ggc  345
59 Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly
60       85                  90                  95
62 ggc cag ggc ttc tcc tac ccc tac aag gcc gtc ttc agt acc cag ggc  393
63 Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
64 100                 105                 110                 115
66 ccc cct ctg gcc agc ctg caa gat agc cat ttc ctc acc gac gcc gac  441
67 Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp
```

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Input Set : A:\Cbm-691.app
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```
68                 120               125                130
70 atg gtc atg agc ttc gtc aac ctc gtg gaa cat gac aag gaa ttc ttc   489
71 Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe
72                 135               140               145
74 cac cca cgc tac cac cat cga gag ttc cgg ttt gat ctt tcc aag atc   537
75 His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile
76          150               155               160
78 cca gaa ggg gaa gct gtc acg gca gcc gaa ttc cgg atc tac aag gac   585
79 Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp
80       165               170               175
82 tac atc cgg gaa cgc ttc gac aat gag acg ttc cgg atc agc gtt tat   633
83 Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr
84 180               185               190               195
86 cag gtg ctc cag gag cac ttg ggc agg gaa tcg gat ctc ttc ctg ctc   681
87 Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu
88                 200               205               210
90 gac agc cgt acc ctc tgg gcc tcg gag gag ggc tgg ctg gtg ttt gac   729
91 Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp
92                 215               220               225
94 atc aca gcc acc agc aac cac tgg gtg gtc aat ccg cgg cac aac ctg   777
95 Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu
96          230               235               240
98 ggc ctg cag ctc tcg gtg gag acg ctg gat ggg cag agc atc aac ccc   825
99 Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro
100      245               250               255
102 aag ttg gcg ggc ctg att ggg cgg cac ggg ccc cag aac aag cag ccc   873
103 Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro
104 260              265               270               275
106 ttc atg gtg gct ttc ttc aag gcc acg gag gtc cac ttc cgc agc atc   921
107 Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile
108                 280               285               290
110 cgg tcc acg ggg agc aaa cag cgc agc cag aac cgc tcc aag acg ccc   969
111 Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro
112                 295               300               305
114 aag aac cag gaa gcc ctg cgg atg gcc aac gtg gca gag aac agc agc   1017
115 Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser
116          310               315               320
118 agc gac cag agg cag gcc tgt aag aag cac gag ctg tat gtc agc ttc   1065
119 Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe
120      325               330               335
122 cga gac ctg ggc tgg cag gac tgg atc atc gcg cct gaa ggc tac gcc   1113
123 Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala
124 340              345               350               355
126 gcc tac tac tgt gag ggg gag tgt gcc ttc cct ctg aac tcc tac atg   1161
127 Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met
128                 360               365               370
130 aac gcc acc aac cac gcc atc gtg cag acg ctg gtc cac ttc atc aac   1209
131 Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn
132              375               380               385
```

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Output Set: N:\CRF3\06282001\I509648.raw

```
134 ccg gaa acg gtg ccc aag ccc tgc tgt gcg ccc acg cag ctc aat gcc   1257
135 Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala
136         390                 395                 400
138 atc tcc gtc ctc tac ttc gat gac agc tcc aac gtc atc ctg aag aaa   1305
139 Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys
140         405                 410                 415
142 tac aga aac atg gtg gtc cgg gcc tgt ggc tgc cac'tagctcctcc        1351
143 Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
144 420                 425                 430
146 gagaattcag accctttggg gccaagtttt tctggatcct ccattgctcg ccttggccag 1411
148 gaaccagcag accaactgcc ttttgtgaga ccttcccctc cctatcccca actttaaagg 1471
150 tgtgagagta ttaggaaaca tgagcagcat atggcttttg atcagttttt cagtggcagc 1531
152 atccaatgaa caagatccta caagctgtgc aggcaaaacc tagcaggaaa aaaaaacaac 1591
154 gcataaagaa aaatggccgg gccaggtcat tggctgggaa gtctcagcca tgcacggact 1651
156 cgtttccaga ggtaattatg agcgcctacc agccaggcca cccagccgtg ggaggaaggg 1711
158 ggcgtggcaa ggggtgggca cattggtgtc tgtgcgaaag gaaaattgac ccggaagttc 1771
160 ctgtaataaa tgtcacaata aaacgaatga atgaaaaaaa aaaaaaaaa a            1822
163 <210> SEQ ID NO: 2
164 <211> LENGTH: 431
165 <212> TYPE: PRT
166 <213> ORGANISM: Homo sapiens
168 <400> SEQUENCE: 2
169 Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
170   1               5                 10                  15
172 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
173             20                  25                  30
175 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
176         35                  40                  45
178 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
179         50                  55                  60
181 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
182   65                  70                  75                  80
184 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
185             85                  90                  95
187 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
188             100                 105                 110
190 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
191         115                 120                 125
193 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
194         130                 135                 140
196 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
197 145                 150                 155                 160
199 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
200                 165                 170                 175
202 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
203             180                 185                 190
205 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
206         195                 200                 205
208 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
```

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Input Set : A:\Cbm-691.app
Output Set: N:\CRF3\06282001\I509648.raw

```
209      210                      215                      220
211 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
212 225                      230                      235                      240
214 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
215                      245                      250                      255
217 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
218                      260                      265                      270
220 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
221          275                      280                      285
223 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
224          290                      295                      300
226 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
227 305                      310                      315                      320
229 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
230                      325                      330                      335
232 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
233          340                      345                      350
235 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
236          355                      360                      365
238 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
239          370                      375                      380
241 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
242 385                      390                      395                      400
244 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
245                      405                      410                      415
247 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
248          420                      425                      430
252 <210> SEQ ID NO: 3
253 <211> LENGTH: 102
254 <212> TYPE: PRT
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Description of Artificial Sequence: OPX -
259       Consensus sequence
261 <220> FEATURE:
262 <223> OTHER INFORMATION: Wherein Xaa is independently selected from a group
263       of one or more specified amino acids as defined in
264       the specification
266 <400> SEQUENCE: 3
```

W--> 267 Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe Xaa Asp Leu Gly Trp Xaa
```
268   1                    5                      10                      15
```
W--> 270 Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
```
271          20                      25                      30
```
W--> 273 Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
```
274          35                      40                      45
```
W--> 276 Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
```
277          50                      55                      60
```
W--> 279 Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
```
280 65                      70                      75                      80
```

Input Set : A:\Cbm-691.app
Output Set: N:\CRF3\06282001\I509648.raw

```
W--> 282 Asp Xaa Ser Xaa Asn Val Xaa Leu Xaa Lys Xaa Arg Asn Met Val Val
     283         85              90              95
W--> 285 Xaa Ala Cys Gly Cys His
     286         100
     289 <210> SEQ ID NO: 4
     290 <211> LENGTH: 97
     291 <212> TYPE: PRT
     292 <213> ORGANISM: Artificial Sequence
     294 <220> FEATURE:
     295 <223> OTHER INFORMATION: Description of Artificial Sequence: Generic
     296       Sequence 7
     298 <220> FEATURE:
     299 <223> OTHER INFORMATION: Wherein Xaa is independently selected from a group
     300       of one or more specified amino acids as defined in
     301       the specification
     303 <400> SEQUENCE: 4
W--> 304 Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa Xaa Xaa Xaa Xaa Xaa
     305 1               5               10              15
W--> 307 Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Pro
     308         20              25              30
W--> 310 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala Xaa Xaa Xaa Xaa Xaa
     311         35              40              45
W--> 313 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Pro
     314     50              55              60
W--> 316 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     317 65              70              75              80
W--> 319 Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa Val Xaa Xaa Cys Xaa Cys
     320             85              90              95
W--> 322 Xaa
     326 <210> SEQ ID NO: 5
     327 <211> LENGTH: 102
     328 <212> TYPE: PRT
     329 <213> ORGANISM: Artificial Sequence
     331 <220> FEATURE:
     332 <223> OTHER INFORMATION: Description of Artificial Sequence: Generic
     333       Sequence 8
     335 <220> FEATURE:
     336 <223> OTHER INFORMATION: Wherein Xaa is independently selected from a group
     337       of one or more specified amino acids as defined in
     338       the specification
     340 <400> SEQUENCE: 5
W--> 341 Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa
     342 1               5               10              15
W--> 344 Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly
     345         20              25              30
W--> 347 Xaa Cys Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala
     348         35              40              45
W--> 350 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     351     50              55              60
```

***Please Note:***
**Use of n and/or Xaa have been detected in the Sequence Listing.  Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.**

**VERIFICATION SUMMARY**                    DATE: 06/28/2001
PATENT APPLICATION:  **US/09/509,648**      TIME: 13:59:50

Input Set : **A:\Cbm-691.app**
Output Set: **N:\CRF3\06282001\I509648.raw**

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L:267 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:267 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:270 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:273 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:273 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:276 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:276 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:279 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:279 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:282 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:282 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:285 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:285 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:304 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:304 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:307 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:307 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:310 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:310 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:313 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:313 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:316 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:316 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:319 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:319 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:322 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:322 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:341 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:341 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:344 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:344 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:344 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
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**VERIFICATION SUMMARY**                          DATE: 06/28/2001
PATENT APPLICATION: **US/09/509,648**             TIME: 13:59:50

Input Set : **A:\Cbm-691.app**
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```
L:347 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:347 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:350 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:350 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:353 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:353 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:356 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:356 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:359 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:359 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:359 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:378 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:378 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:381 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:381 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:384 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:384 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:387 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:387 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:390 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:393 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:415 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:421 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:473 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
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